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November 13, 2000

Attorney Docket No.: 07419-030001

Box Patent Application
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Presented for filing is a new continuation-in-part patent application of:

Applicant: EISENBERG ET AL.

Title: DETERMINING THE FUNCTIONS AND INTERACTIONS OF
PROTEINS BY COMPARATIVE ANALYSIS

Enclosed are the following papers, including those required to receive a filing date
under 37 CFR §1.53(b):

	<u>Pages</u>
Specification	192
Claims	7
Abstract	1
Declaration	[To be Filed at a Later Date]
Drawing(s)	5

Enclosures:

— Postcard.

This application is a continuation-in-part (and claims the benefit of priority under 35 USC §120) of U.S. application serial no. PCT/US00/02246, filed January 28, 2000, and this application claims the benefit of priority under 35 U.S.C. § 119(e) of U.S. Provisional Application Nos. 60/165,124 and 60/165,086, both filed November 12, 1999, and U.S. Provisional Application No. 60/179,531, filed February 1, 2000.

CERTIFICATE OF MAILING BY EXPRESS MAIL

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I hereby certify under 37 CFR §1.10 that this correspondence is being deposited with the United States Postal Service as Express Mail Post Office to Addressee with sufficient postage on the date indicated below and is addressed to the Commissioner for Patents, Washington, D.C. 20231.

Date of Deposit November 13, 2000

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International Application Serial No. PCT/US00/02246 claims the benefit of priority under 35 U.S.C. § 119(e) of U.S. Provisional Application Serial No. 60/117,844, filed January 29, 1999, U.S. Provisional Application Serial No. 60/118,206, filed February 1, 1999, U.S. Provisional Application Serial No. 60/126,593, filed March 26, 1999, U.S. Provisional Applications Serial No. 60/134,093, filed May 14, 1999, and U.S. Provisional Application Serial No. 60/134,092, filed May 14, 1999. The disclosure of each of the aforementioned applications is considered part of (and is incorporated by reference in) the disclosure of this application.

This applicant is entitled to Small Entity Status.

Basic filing fee	\$355
Total claims in excess of 20 times \$9	\$207
Independent claims in excess of 3 times \$40	\$80
Fee for multiple dependent claims	\$135
Total filing fee:	\$777

A check for the filing fee is enclosed. Please apply any other required fees or any credits to deposit account 06-1050, referencing the attorney docket number shown above.

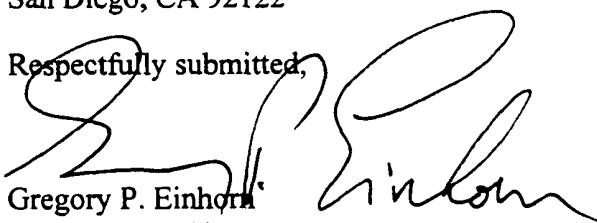
If this application is found to be incomplete, or if a telephone conference would otherwise be helpful, please call the undersigned at (858) 678-5070.

Kindly acknowledge receipt of this application by returning the enclosed postcard.

Please send all correspondence to:

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Respectfully submitted,


Gregory P. Einhorn
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Enclosures
GPE/mc
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DETERMINING THE FUNCTIONS AND INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS

Related Applications

The present application is a continuation-in-part application ("CIP") of Patent
5 Convention Treaty (PCT) International Application Serial No: PCT/US00/02246, filed in the
U.S. receiving office on January 28, 2000, and this application claims the benefit of priority
under 35 U.S.C. § 119(e) of U.S. Provisional Application Nos. 60/165,124, and 60/165,086,
both filed November 12, 1999, and U.S. Provisional Application No. 60/179,531, filed February
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Applications Serial No. 60/134,093, filed May 14, 1999, and U.S. Provisional Application
Serial No. 60/134,092, filed May 14, 1999. Each of the aforementioned applications is
15 explicitly incorporated herein by reference in their entirety and for all purposes.

TECHNICAL FIELD

This invention generally relates to genetics and microbiology. The invention
provides novel methods to identify the function of and relationships between nucleic acid and
protein sequences. The method is particularly useful for finding the identifying genes and
20 polypeptides having potential therapeutic relevance in organisms, e.g., microorganisms, such
as *Mycobacterium tuberculosis*. The invention also provides *Mycobacterium tuberculosis*
genes and polypeptides found by these methods. These genes and polypeptides are useful as
potential drug targets.

BACKGROUND

25 The determination of the functions of and relationships between nucleic acid
and protein sequences has traditionally relied on either the study of homology and sequence
identity with genes and proteins of known function or, in the absence of informative
homology, laborious experimental work. The availability of many complete genome
sequences has made it possible to develop new strategies for computational determination of
30 protein functions. Several methods have been developed which can predict the general